

[illegible]

Query Match 2.5% Score 8; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy (320) 223 ALASISV 230
Db (613) 98 ALASISV 105

RESULT 7
MUTL_CHLTP STANDARD; PRT; 624 AA.
ID Q88AX3;
AC Q88AX3;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA mismatch repair protein mutL.
GN MUTL OR CT2028
OS Chlorobium tepidum.
OC Bacteria; Chlorobii; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A. 49552 / DSM 12025;
RX STRAIN=ILS / ATCC 49552 / DSM 12025;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.P., Wu M.,
RA Dodson R.J., Deboy R., Gwin M.N., Nelson M.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Newman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathevan J., Khouri H., White O., Gruber T.M., Kechum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.,
RA "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
CC -1- FUNCTION: This protein is involved in the repair of mismatches in
CC DNA. It is required for dam-dependent methyl-directed DNA mismatch
CC repair. May act as a "molecular matchmaker", a protein that
CC promotes the formation of a stable complex between two or more
CC DNA-binding proteins in an ATP-dependent manner without itself
CC being part of a final effector complex (by similarity).
CC -1- SIMILARITY: Belongs to the DNA mismatch repair mutL/hexB family.

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EMBL; AE012953; AA073245.1;
DR TIGR; CT2028;
DR HAMAP; MF_00149;
DR InterPro; IPR003594; ATPbind_Atpase.
DR InterPro; IPR002099; DNA_mis_repair.
DR Pfam; PF01119; DNA_mis_repair; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR SMART; SM00387; HATPase_c; 1.
DR TIGRFAMs; TIGR00585; mutL; 1.
DR PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
KW DNA repair; Complete proteome.
SQ SEQUENCE 624 AA; 69836 MW; 43F3CE8234A42CFF CRC64;

Query Match 2.5% Score 8; DB 1; Length 624;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 223 ALASISV 230
Db 99 ALASISV 105

RESULT 8
MUTL_HABIN STANDARD; PRT; 629 AA.
ID P44354;
AC P44354;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 08-FEB-2003 (Rel. 41, Last annotation update)
DE DNA mismatch repair protein mutL.
GN MUTL OR H10067.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A. 29420 / ATCC 51907;
RX STRAIN=Hd / KM20 / ATCC 51907;
RA MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Sult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McInerney K., Sutton G., Fitchugh W., Field C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RL Science 269:496-512 (1995).
CC -1- FUNCTION: This protein is involved in the repair of mismatches in
CC DNA. It is required for dam-dependent methyl-directed DNA mismatch
CC repair. May act as a "molecular matchmaker", a protein that
CC promotes the formation of a stable complex between two or more
CC DNA-binding proteins in an ATP-dependent manner without itself
CC being part of a final effector complex (by similarity).
CC -1- SIMILARITY: Belongs to the DNA mismatch repair mutL/hexB family.

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or send an email to license@isb-sib.ch).

EMBL; U32692; AAC21745.1;
DR PIR; P64046; E64046.
DR KSSP; P23367; I8XN.
DR TIGR; H10067;
DR HAMAP; MF_00149;
DR InterPro; IPR003594; ATPbind_Atpase.
DR InterPro; IPR002099; DNA_mis_repair.
DR Pfam; PF01119; DNA_mis_repair; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR SMART; SM00387; HATPase_c; 1.
DR TIGRFAMs; TIGR00585; mutL; 1.
DR PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
KW DNA repair; Complete proteome.
SQ SEQUENCE 629 AA; 71622 MW; 0ADC240FD94D1556 CRC64;

Query Match 2.5% Score 8; DB 1; Length 629;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 223 ALASISV 230
Db 98 ALASISV 105

RESULT 9
MUTL_PSEPK STANDARD; PRT; 632 AA.
ID MUTL_PSEPK
AC Q88DD1;